SCORE Search Results Details for Application 10563896 and Search Result 20080416_145120_us-10-563-896-3.rag.

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This page gives you Search Results detail for the Application 10563896 and Search Result 20080416 145120 us-10-563-896-3.rag.

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OM protein - protein search, using sw model

April 16, 2008, 14:55:47 ; Search time 120 Seconds Run on:

(without alignments)

1705.326 Million cell updates/sec

Title: US-10-563-896-3

Perfect score: 1807

Sequence: 1 MGKSKEISQDLRKKIVDLHK......EGYPKRLTQVKQFKGNATKY 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3405708 segs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A_Geneseq_200711:* Database :

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*

6: geneseqp2003a:*

7: geneseqp2003b:*

8: geneseqp2004a:*

9: geneseqp2004b:*

10: genesegp2005:*

11: genesegp2006:*

12: genesegp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		્ર				
Result		Query				
No.	Score		Length	DB	ID	Description
1	1807	100.0	340	2	AAW68520	Aaw68520 Salmonid-
2	1807	100.0	340	2	AAY17440	Aay17440 SB transp
3	1807	100.0	340	4	AAY72024	Aay72024 SB (Sleep
4	1807	100.0	340	5	AAG80595	Aag80595 Sleeping
5	1807	100.0	340	5	ABB07570	Abb07570 SB transp
6	1807	100.0	340	6	ABB99719	Abb99719 Amino aci
7	1807	100.0	340	7	ADD41924	Add41924 Amino aci
8	1807	100.0	340	10	ADW22678	Adw22678 Sleeping
9	1807	100.0	340	10	ADW03280	Adw03280 Sleeping
10	1807	100.0	340	11	AEF81669	Aef81669 Salmonid
11	1807	100.0	340	12	AEP47151	Aep47151 SB transp
12	1802	99.7	340	7	ADK17480	Adk17480 Salmonid
13	1787	98.9	340	11	AEF81683	Aef81683 Salmonid
14	1786	98.8	340	4	AAB47211	Aab47211 Sleeping
15	1786	98.8	340	10	ADW46561	Adw46561 Salmonid
16	1786	98.8	340	12	AEL92393	Ael92393 Sleeping
17	1784	98.7	340	11	AEF81684	Aef81684 Salmonid
18	1783	98.7	340	10	ADW46599	Adw46599 Salmonid
19	1783	98.7	340	10	ADW46649	Adw46649 Salmonid
20	1783	98.7	340	10	ADW46612	Adw46612 Salmonid
21	1783	98.7	340	10	ADW46621	Adw46621 Salmonid
22	1783	98.7	340	10	ADW46613	Adw46613 Salmonid
23	1782	98.6	340	10	ADW46626	Adw46626 Salmonid
24	1782	98.6	340	10	ADW46644	Adw46644 Salmonid
25	1782	98.6	340	10	ADW46614	Adw46614 Salmonid
26	1782	98.6	340	10	ADW46597	Adw46597 Salmonid
27	1782	98.6	340	10	ADW46587	Adw46587 Salmonid
28	1781	98.6	340	10	ADW46656	Adw46656 Salmonid
29	1781	98.6	340	10	ADW46591	Adw46591 Salmonid
30	1781	98.6	340	10	ADW46643	Adw46643 Salmonid
31	1781	98.6	340	10	ADW46658	Adw46658 Salmonid
32	1781	98.6	340	10	ADW46588	Adw46588 Salmonid
33	1781	98.6	340	10	ADW46605	Adw46605 Salmonid
34	1781	98.6	340	10	ADW46603	Adw46603 Salmonid
35	1781	98.6	340	10	ADW46653	Adw46653 Salmonid
36	1781	98.6	340	10	ADW46607	Adw46607 Salmonid
37	1781	98.6	340	10	ADW46615	Adw46615 Salmonid
38	1781	98.6	340	10	ADW46617	Adw46617 Salmonid
39	1781	98.6	340	10	ADW46590	Adw46590 Salmonid
40	1781	98.6	340	10	ADW46593	Adw46593 Salmonid
41	1781	98.6	340	10	ADW46608	Adw46608 Salmonid
42	1781	98.6	340	10	ADW46645	Adw46645 Salmonid
43	1781	98.6	340	10	ADW46601	Adw46601 Salmonid
4 4	1781	98.6	340	10	ADW46610	Adw46610 Salmonid
45	1781	98.6	340	10	ADW46630	Adw46630 Salmonid

ALIGNMENTS

RESULT 1 AAW68520

ID AAW68520 standard; protein; 340 AA.

XX

```
AC
    AAW68520;
XX
DT
     27-AUG-2003 (revised)
DT
     25-JAN-1999 (first entry)
XX
DE
     Salmonid-type Tc1-like transposase protein.
XX
KW
     Transposase; salmonid; Tc1-like family; homology; vertebrate; transposon;
KW
     zebrafish; gene transfer; gene therapy; inverted repeat; direct repeat;
KW
     genome.
XX
OS
    transposons.
XX
FH
                     Location/Qualifiers
     Key
FT
     Domain
                    11. .61
                     /note= "Paired-like domain with Leucine Zipper"
FT
FT
     Domain
                     104. .105
FT
                     /note= "form part of a bipart nuclear localisation
                     signal"
FT
FT
                     116. .120
     Domain
FT
                     /note= "form part of a bipart nuclear localisation
FT
                     signal"
FT
                     151. .161
     Domain
FT
                     /note= "DD(34)E box"
FT
    Region
                     183. .198
FT
                     /note= "Glycine-rich box"
FT
     Domain
                     241. .251
FT
                     /note= "DD(34)E box"
FT
                     268. .282
     Domain
                     /note= "DD(34)E box"
FT
XX
PN
    WO9840510-A1.
XX
PD
    17-SEP-1998.
XX
PF
    11-MAR-1998; 98WO-US004687.
XX
PR
    11-MAR-1997; 97US-0040664P.
PR
     28-JUL-1997;
                   97US-0053868P.
PR
    13-NOV-1997; 97US-0065303P.
XX
     (MINU ) UNIV MINNESOTA.
PA
XX
PΙ
     Hackett PB, Ivics Z, Izsvak Z, Caldovic L;
XX
DR
    WPI; 1998-531525/45.
DR
    N-PSDB; AAV33841.
XX
PΤ
    New isolated transposase gene - used to develop products for the
PT
     integration of nucleic acid fragments into the nucleic acid of cells,
PT
    particularly for gene therapy.
XX
PS
     Disclosure; Fig 2B; 79pp; English.
XX
CC
     This sequence represents a novel transposase protein of the salmonid-type
CC
     Tc1-like family. The coding sequence was reconstructed based on sequence
CC
    homology between members of the Tc1-like family of vertebrate
CC
    transposons, especially based on the sequence of a number of fish, e.g.
CC
     zebrafish transposons. The transposase can be used in a gene transfer
CC
    method, especially for gene therapy treatment, by flanking a heterologous
CC
     gene to be expressed in a cell with the inverted or direct repeat
```

```
CC
    sequences to which the transposase binds. This allows the transposase-
CC
   mediated transposition of the heterologous into the genome of the host
CC
   cell. (Updated on 27-AUG-2003 to correct OS field.)
XX
SO
   Sequence 340 AA;
                    100.0%; Score 1807; DB 2;
 Query Match
                                           Length 340;
 Best Local Similarity
                    100.0%; Pred. No. 2.4e-156;
 Matches 340; Conservative
                         0; Mismatches
                                        0; Indels
                                                   0; Gaps
                                                            0;
         1 MGKSKEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKHHGTTQPSYRSGR 60
Qу
           1 MGKSKEISODLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKHHGTTQPSYRSGR 60
        61 RRVLSPRDERTLVRKVOINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKK 120
Qу
           61 RRVLSPRDERTLVRKVQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKK 120
Db
Qу
       121 PLLQNRHKKARLRFATAHGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKN 180
           121 PLLONRHKKARLRFATAHGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKN 180
Db
       181 TIPTVKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKLKLGRKWV 240
Qу
           181 TIPTVKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKLKLGRKWV 240
        241 FOMDNDPKHTSKVVAKWLKDNKVKVLEWPSOSPDLNPIENLWAELKKRVRARRPTNLTQL 300
Qу
           241 FQMDNDPKHTSKVVAKWLKDNKVKVLEWPSQSPDLNPIENLWAELKKRVRARRPTNLTQL 300
Db
       301 HQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY 340
Qv
           301 HQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY 340
Db
```